

Access DB# 117502

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>[Signature]</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #: <u>122504</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>3/23</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>3/24</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>15</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>+15</u>	Other _____	Other (specify) _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 117502

TO: Phillip Gambel
Location: 3e81 / 3c70
Wednesday, March 24, 2004
Art Unit: 1644
Phone: 272-0844
Serial Number: 09 / 955866

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504
jan.delaval@uspto.gov

Search Notes

17502

Delaval, Jan

From: Gambel, Phillip
Sent: Tuesday, March 23, 2004 9:51 AM
To: Delaval, Jan
Subject: FW: roark amendment for new examiner 09/955,866

Subject: roark amendment for new examiner **09/955,866**

Jan

Please perform a sequence and a sequence interference search for

USSN 09 / 955,866 (roark amendment for new examiner)

- 1) SEQ ID NO: 1
- 2) SEQ ID NO: 1 as an "oligo"
- 3) SEQ ID NO: 2
- 4) SEQ ID NO: 2 as an "oligo"

Thanx

Phillip Gambel
Art Unit 1644
272-0844

1644 mailbox 3c70

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RESULT 2

US-09-620-461-1
; Sequence 1, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(2229)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: CDS
; LOCATION: (78)...(896)
; NAME/KEY: misc.feature
; LOCATION: (1)...(2229)
; OTHER INFORMATION: B7-2H Long

US-09-620-461-1

Query Match 98.5%; Score 1191; DB 4; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 919 AAGAAATCGGTGGCTGACAGGCTTGGCAATTTGGCACTTTTCAATGCTTGGATGACCC 978
Db 964 AAGAAATCGGTGGCTGACAGGCTTGGCAATTTGGCACTTTTCAATGCTTGGATGACCC 1023
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RESULT 3

US-09-910-174B-20
; Sequence 20, Application US/09910174B

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 01:43:25 ; Search time 462 Seconds
(without alignments)
9680.252 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2438257 seqs, 1849576744 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : Published Applications NA:*

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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1209	100.0	1209	9	US-09-955-866-1
2	1191	98.5	2229	9	US-09-910-174A-1
3	1191	98.5	2242	10	US-09-814-353-21297
4	1191	98.5	2435	9	US-09-875-338-14
5	1191	98.5	2435	15	US-10-077-023-14
6	1155	95.5	2200	15	US-10-120-988-309
7	1140	94.3	2386	14	US-10-041-319-4
8	964	79.7	1223	9	US-09-895-837-1
9	964	79.7	1223	9	US-09-896-913A-1
10	964	79.7	1223	15	US-10-034-650-41
11	891	73.7	2406	15	US-10-023-339-3
12	823	68.1	842	9	US-09-875-338-20
13	823	68.1	842	14	US-10-077-023-20
14	822	68.0	822	14	US-10-041-319-5
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16	819	67.7	819	9	US-09-794-210-1	Sequence 1, Appli
17	819	67.7	819	9	US-09-910-174A-20	Sequence 20, Appli
18	819	67.7	819	9	US-09-895-837-3	Sequence 3, Appli
19	819	67.7	819	9	US-09-896-913A-3	Sequence 3, Appli
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21	600	49.6	1356	14	US-10-077-023-16	Sequence 16, Appli
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24	361	29.9	19217	9	US-09-910-174A-21	Sequence 21, Appli
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26	361	29.9	79684	15	US-10-034-650-40	Sequence 40, Appli
27	330	27.3	401	9	US-09-735-705-264	Sequence 264, App
28	330	27.3	401	9	US-09-850-716A-264	Sequence 264, App
29	330	27.3	401	9	US-09-897-778-264	Sequence 264, App
30	330	27.3	401	14	US-10-117-982-264	Sequence 264, App
31	330	27.3	401	15	US-10-313-986-264	Sequence 264, App
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33	309	25.6	9179	9	US-09-955-866-16	Sequence 16, Appli
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35	285	23.6	786	15	US-10-023-339-11	Sequence 11, Appli
36	274	22.7	1814	9	US-09-955-866-17	Sequence 17, Appli
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73	21	1.7	482	10	US-09-918-995-15964	Sequence 15964, A
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85	19	1.6	522	14	US-10-060-036-3187	Sequence 3187, Ap
86	19	1.6	650	15	US-10-027-632-193797	Sequence 193797, A
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88	19	1.6	661	14	US-10-092-154-278	Sequence 278, App

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C 101	19	1.6	484	4	AAS58643	cDNA #131
C 102	19	1.6	522	6	ABV97779	Human pan
C 103	19	1.6	591	2	AAT68111	H. pylori
C 104	19	1.6	661	4	ABK41880	cDNA enco
C 105	19	1.6	661	8	ADB59547	Connectiv
C 106	19	1.6	748	2	AAV69478	Banana fr
C 107	19	1.6	842	5	AS83126	DNA enco
C 108	19	1.6	939	2	AAV30464	H. pylori
C 109	19	1.6	1008	2	AAV30438	H. pylori
C 110	19	1.6	1060	3	AAC59683	Human sec
C 111	19	1.6	1588	4	AAD08388	Human sec
C 112	19	1.6	1588	7	ABZ73347	Secreted
C 113	19	1.6	1588	9	ADC20104	Human sec
C 114	19	1.6	1650	2	AAZ33598	Human bre
C 115	19	1.6	1682	6	ABZ17147	Arabidops
C 116	19	1.6	1725	3	AAZ52367	NSQ gene
C 117	19	1.6	1725	6	AAZ42463	Human mat
C 118	19	1.6	1756	9	ABZ73862	Secreted
C 119	19	1.6	1756	9	ADC20642	Human sec
C 120	19	1.6	2013	6	ABK46114	cDNA enco
C 121	19	1.6	2087	4	AAH44395	Human CDN
C 122	19	1.6	2420	4	AAZ26460	Human bre
C 123	19	1.6	2421	4	AAZ26449	Human bre
C 124	19	1.6	6480	7	ABZ67665	Human sec
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C 126	19	1.6	75395	7	ABX93648	Human Gen
C 127	19	1.6	83946	6	ABQ88101	Human ost
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C 129	19	1.6	110000	6	ABX08336	Continuation (10 of
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C 132	18	1.5	18	6	ABK24075	B7-relate
C 133	18	1.5	18	6	ABK24068	B7-relate
C 134	18	1.5	18	6	ABK24073	B7-relate
C 135	18	1.5	18	6	ABK24078	B7-relate
C 136	18	1.5	26	6	ABK24091	B7-relate
C 137	18	1.5	101	9	ADD27953	Canine CO
C 138	18	1.5	302	4	AAI83753	Human pol
C 139	18	1.5	392	8	ACH18938	Human adu
C 140	18	1.5	524	6	ABN73636	Bovine em
C 141	18	1.5	557	6	AAZ41728	Murine ri
C 142	18	1.5	635	4	AAI80602	Human pol
C 143	18	1.5	728	6	ABZ77512	Frog embr
C 144	18	1.5	775	4	AAI95488	Human neu
C 145	18	1.5	868	2	AAV37523	Human sec
C 146	18	1.5	1117	4	AAH48396	Fumarase
C 147	18	1.5	1157	7	ABX90530	Human CDN
C 148	18	1.5	1223	7	AAZ54709	Mouse SCR
C 149	18	1.5	1338	7	ACA21558	Prokaryot
C 150	18	1.5	1422	4	ABL13999	Drosophil

osteoarthritis; immune thrombocytopaenic purpura; ITP; antibacterial; Hashimoto's thyroiditis; diabetes mellitus; graft survival; tumour; immune cell activation; immunosuppressive; vasotropic; gene therapy; gynaecological; rheumatoid arthritis; cytostatic; Grave's disease; dermatological; gene; ds.

Homo sapiens.

Key	Location/Qualifiers
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WO200224891-A2.

28-MAR-2002.

19-SEP-2001; 2001WO-US029183.

20-SEP-2000; 2000US-0233867P.

(AMGE-) AMGEN INC.

Fox M, Sullivan JK, Holst P, Yoshinaga SK;

WPI; 2002-416284/44.

P-PSDB; AAE23073.

Novel B7-like (B7-L) polypeptides and nucleic acids encoding the polypeptides, useful for diagnosing, treating and preventing endometriosis, infertility, cancer, rheumatoid arthritis, multiple myeloma.

Claim 1; Fig 1; 18app; English.

The invention relates to B7-like (B7-L) polypeptides and nucleic acids encoding them. The invention also relates to selective binding agents, vectors, host cells and methods for producing B7-L polypeptides. B7-L gene, protein and selective binding agents are useful for treating, preventing, ameliorating a B7-L polypeptide-related disease, condition or disorder. B7-L agonist and antagonist are useful for diagnosis or treatment of diseases associated with abnormal cell proliferation, e.g. arteriosclerosis and vascular restenosis, diseases associated with reproductive system such as infertility, miscarriage, pre-term labour and delivery or endometriosis. B7-L gene, protein and its agonist or antagonist are useful for treating, diagnosing, ameliorating diseases associated with T-cell function, autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, immune thrombocytopenic purpura (ITP) and psoriasis, Hashimoto's thyroiditis, Grave's disease, or diabetes mellitus), graft survival, immune cell activation or inhibiting tumour cell growth, T-cell dependent B-cell mediated diseases and cancer gene immunotherapy. The present sequence is human B7-L gene

Sequence 1209 BP; 354 A; 325 C; 250 G; 280 T; 0 U; 0 Other;

Query Match 100.0%; Score 1209; DB 6; Length 1209;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	TGGAATTGCAGCTTCCACGATAGCAGCTTTATTCAGTGACAGTCCCTAAGAACTGT	120

Human; B7-L protein; cell proliferation; arteriosclerosis; cancer; vascular restenosis; reproductive system; infertility; miscarriage; pre-term labour; delivery; endometriosis; T-cell function; psoriasis; autoimmune disease; systemic lupus erythematosus; antiinflammatory;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 22:59:39 ; Search time 516 Seconds

(without alignment)
9953.627 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

Sequence: 1 cagaagagacattatgat.....agtttttaagtgatttoca 1209

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1209	100.0	1209	6	AAD36968 Human B7-
2	1191	98.5	2229	6	AAD30541 Human B7-
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4	1191	98.5	2386	7	AAD48356 Human B7-
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6	1155	95.5	2200	7	ABX71082 Novel hum
7	1140	94.3	2386	7	AAD48333 Human B7-
8	1089	90.1	2386	7	AAD48354 Human B7-
9	964	79.7	1223	6	AAD27371 Human PD-
10	964	79.7	1223	6	AAL41871 Human PD-
11	964	79.7	1223	7	ABT14005 Human PD-
12	964	79.7	1223	7	ABX13050 Human PD-
13	964	79.7	1223	8	ADA03075 Human hCG
14	964	79.7	1223	8	ADA66359 Human hCG
15	964	79.7	1223	9	ADB72813 Human hCG
16	891	73.7	2406	4	AAD05220 Human sec
17	891	73.7	2406	6	AAD32520 Human B7-
18	891	73.7	2406	7	ADA55940 Gene enco
19	823	68.1	842	6	ABK24021 B7-relate
20	822	68.0	822	7	AAD48353 Human B7-
21	822	68.0	822	8	ADA03076 Human hCG
22	822	68.0	822	8	ADA66360 Human hCG
23	822	68.0	822	9	ADB72814 Human hCG

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25	819	67.7	819	6	ABK88228	DNA encod
26	819	67.7	819	6	AAI70887	Human co-
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38	361	29.9	1921	6	AAD36973	Human B7-
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44	330	27.3	401	6	ABQ92365	Human lun
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46	324	26.8	560	6	ABS52109	Human but
47	309	25.6	9179	6	AAD36971	Human B7-
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72	25	2.1	34	6	ABK24082	B7-relate
73	25	2.1	34	6	ABK24090	B7-relate
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c 83	22	1.8	22	6	AAL41882	Human PD-
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ALIGNMENTS

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VERSION CA489316.1 GI:24952107
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 906)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgi.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gagbs-x@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14283 row: d column: 19
High quality sequence stop: 593.

FEATURES
Location/Qualifiers
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/note="Vector: pCMW-SORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
Insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN
Query Match 52.5%; Score 635; DB 14; Length 906;
Best Local Similarity 99.9%; Pred. No. 7.3e-310;
Matches 685; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 128 AGAGCATGGCAGCAATGTGACCTCGAAATGCAACTTTTGACACTGGAAGTCATGTGAACCT 187
Db 61 AGAGCATGGCAGCAATGTGACCTCGAAATGCAACTTTTGACACTGGAAGTCATGTGAACCT 120

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QY 248 AGCCACTTTGCTGGAGGACGCTGCCCTTAGGGAGGCGCTGTTCCACATACCTCAAGT 307
Db 181 AGCCACTTTGCTGGAGGACGCTGCCCTTAGGGAGGCGCTGTTCCACATACCTCAAGT 240

QY 308 CCAAGTGGAGGACGAGACAGTACAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 367

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 00:06:30 ; Search time 2997 Seconds

(without alignments)
12046.505 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

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8: em_htc:*

9: gb_est1:*

10: gb_est2:*

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13: gb_est4:*

14: gb_est5:*

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17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_nus:*

24: em_gss_pro:*

25: em_gss_rpd:*

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	232	19.2	940	13	BO880729
6	228	18.9	502	13	EX280151
7	199	16.5	279	9	AA303575
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c 9	170	14.1	356	10	AW889458
c 10	148	12.2	526	28	AO691335
c 11	123	10.2	775	14	CB312518
c 12	105	8.7	240	9	AA247128
c 13	105	8.7	404	9	AA247117
c 14	99	8.2	573	9	AI762460
c 15	91	7.5	390	9	AA036918
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c 22	22	1.8	1029	13	BU746079
c 23	21	1.7	93	28	AZ812514
c 24	21	1.7	314	14	T05423
c 25	21	1.7	332	10	BE111013
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c 27	21	1.7	456	14	CB545564
c 28	21	1.7	750	14	CF744925
c 29	21	1.7	771	10	BE883693
c 30	21	1.7	799	14	W28577
c 31	21	1.7	849	13	BQ231790
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c 33	21	1.7	868	12	BG282544
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c 35	21	1.7	1018	10	BE962915
c 36	21	1.7	1059	12	BM464169
c 37	21	1.7	1134	12	BM461393
c 38	20	1.7	250	9	AI758557
c 39	20	1.7	286	9	AI272169
c 40	20	1.7	385	29	CE357725
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c 145 16 1.3 4550 4 US-09-218-207-182 Sequence 182, App
c 146 16 1.3 4849 4 US-09-620-312D-39 Sequence 39, Appl
c 147 16 1.3 5214 4 US-09-546-934-2 Sequence 2, Appl
c 148 16 1.3 5643 1 US-08-144-602B-4 Sequence 4, Appl
c 149 16 1.3 6337 4 US-09-620-312D-1063 Sequence 1063, Ap
c 150 16 1.3 8285 4 US-09-732-025-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-910-174B-1
; Sequence 1, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2003-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2229)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)...(896)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2229)
; OTHER INFORMATION: B7-H2 Long
US-09-910-174B-1

Query Match 98.5%; Score 1191; DB 4; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 64 ATCAATACAGAACATGATCTTCCTCTCTGCTAATGTGAGCTGGAAATTCAGCTTCACC 123
QY 79 AGATAGCAGCTTTATTCACAGTGACAGTCCCTTAAGGAACCTGTACATATAGAGCATGGCA 138
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QY 199 CAGCCAGTTTGCAGAAAGTGGAAATGATATACATCCCAACACCGTGAAGAGCACTTTGC 258
Db 244 CAGCCAGTTTGCAGAAAGTGGAAATGATATACATCCCAACACCGTGAAGAGCACTTTGC 303
QY 259 TGGAGGACAGCTGCCCTTAGGAGGCTCTGTTCCACATACCTCAAGTCCAAAGTGAGGG 318
Db 304 TGGAGGACAGCTGCCCTTAGGAGGCTCTGTTCCACATACCTCAAGTCCAAAGTGAGGG 363
QY 319 AGAAGGACAGTACCAATGCAATATCTATGAGGCTGCGCTGGAGTACAGTACCTGA 378
Db 364 AGAAGGACAGTACCAATGCAATATCTATGAGGCTGCGCTGGAGTACAGTACCTGA 423
QY 379 CTCTGAAGTCAAAAGCTTCTTACAGGAAATAAACACTCACATCTCTAAAGTTCCAGAAA 438
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QY 799 ACACNACAAAAGACCTGTCTCCACCAACAAAGAGGGAAGTGAACAGTGTCTATCTGAACT 858

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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 00:04:09 ; Search time 117 Seconds
(without alignments)
5734.493 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1191	98.5	2229	4	US-09-910-174B-1
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4	819	67.7	819	4	US-09-910-174B-20
5	546	45.2	1975	4	US-09-910-174B-3
6	546	45.2	1975	4	US-09-910-174B-3
7	361	29.9	549	4	US-09-910-174B-21
8	361	29.9	549	4	US-09-910-174B-21
9	330	27.3	401	4	US-09-643-597-264
10	330	27.3	401	4	US-09-480-884A-264
11	330	27.3	401	4	US-09-542-615A-264
12	330	27.3	401	4	US-09-606-421B-264
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14	21	1.7	38	4	US-09-910-174B-25
15	21	1.7	38	4	US-09-910-174B-25
16	20	1.7	34	4	US-09-910-174B-26
17	20	1.7	34	4	US-09-910-174B-26
18	19	1.6	73395	4	US-09-984-890-3
19	18	1.5	2160	4	US-09-716-129-12
20	17	1.4	379	4	US-09-621-976-13874
21	17	1.4	466	4	US-09-621-976-1443
22	17	1.4	477	4	US-09-519-232-49
23	17	1.4	491	4	US-09-621-976-17688
24	17	1.4	498	4	US-09-519-232-31
25	17	1.4	498	4	US-09-519-232-47
26	17	1.4	591	2	US-08-704-473-1
27	17	1.4	594	3	US-09-328-111-257
28	17	1.4	597	4	US-09-489-039A-2817
29	17	1.4	612	3	US-09-385-982-400
30	17	1.4	744	4	US-09-252-991A-11267
31	17	1.4	918	4	US-09-711-164-223
32	17	1.4	1105	4	US-09-635-872A-17
33	17	1.4	1105	4	US-09-636-077A-17
34	17	1.4	1105	4	US-09-636-060C-17
35	17	1.4	1105	4	US-09-986-552-17
36	17	1.4	1108	2	US-08-852-807-2
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47	17	1.4	13674	2	US-08-852-807-1
48	17	1.4	64467	4	US-09-803-671B-3
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51	16	1.3	245	6	5187153-26
52	16	1.3	246	4	US-09-107-532A-1078
53	16	1.3	270	4	US-09-134-000C-116
54	16	1.3	282	4	US-09-489-039A-2589
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68	16	1.3	405	1	US-08-259-372A-11
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71	16	1.3	514	4	US-09-621-976-1372
72	16	1.3	558	2	US-08-938-975-1
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74	16	1.3	558	4	US-09-322-379-1
75	16	1.3	593	4	US-09-679-686B-7
76	16	1.3	606	4	US-09-134-001C-2722
77	16	1.3	684	4	US-09-702-705-1441
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79	16	1.3	684	4	US-09-614-124B-1441
80	16	1.3	684	4	US-09-671-325-1441
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85	16	1.3	730	4	US-09-736-457-143
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87	16	1.3	730	4	US-09-671-325-143
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90	16	1.3	889	4	US-08-956-171E-1190
91	16	1.3	909	4	US-09-489-039A-5113
92	16	1.3	915	4	US-09-328-352-3290
93	16	1.3	954	4	US-09-479-614-19
94	16	1.3	954	4	US-09-479-614-21
95	16	1.3	1000	4	US-09-023-655-1428
96	16	1.3	1001	4	US-09-533-029-45
97	16	1.3	1006	4	US-08-956-171E-386
98	16	1.3	1059	4	US-09-134-000C-115
99	16	1.3	1152	3	US-09-188-930-42
100	16	1.3	1152	3	US-09-188-930-211

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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 00:02:04 ; Search time 4686 Seconds
(without alignments)
11182.614 Million cell updates/sec

Title: US-09-955-866-1

Perfect score: 1209

Sequence: 1 cagaagagacacatgat.....agtttttaagtattcca 1209

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Searched: 3470272 seqs, 21671516995 residues

Word size : 0

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1191	98.5	2229	6	AR411237	AR411237 Sequence
5	1191	98.5	2229	6	AX370286	AX370286 Sequence
6	1191	98.5	2435	6	AX357968	AX357968 Sequence
7	1140	94.3	2386	6	AX698931	AX698931 Sequence
8	964	79.7	1223	6	AX420002	AX420002 Sequence
9	964	79.7	1223	6	AX460797	AX460797 Sequence
10	964	79.7	1223	6	AX695966	AX695966 Sequence
11	964	79.7	1223	9	AF344424	AF344424 Homo sapi
12	823	68.1	842	6	AX357974	AX357974 Sequence
13	822	68.0	822	6	AX695967	AX695967 Sequence
14	822	68.0	822	6	AX698932	AX698932 Sequence
15	822	68.0	822	9	AY254343	AY254343 Homo sapi
16	819	67.7	819	6	AR407783	AR407783 Sequence
17	819	67.7	819	6	AR411239	AR411239 Sequence
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19	819	67.7	819	6	AX370305	AX370305 Sequence
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21	819	67.7	819	6	AX460799	AX460799 Sequence
22	819	67.7	819	6	BD161902	BD161902 Novel den
23	779	64.4	1819	6	AX877717	AX877717 Sequence
24	779	64.4	1819	6	BD156810	BD156810 Primer fo
25	779	64.4	1819	9	AK001872	AK001872 Homo sapi
26	600	49.6	1356	6	AX357970	AX357970 Sequence
27	558	46.2	793	6	AX869415	AX869415 Sequence
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35	361	29.9	19217	6	AX411791	AX411791 Sequence
36	361	29.9	79684	6	AX695965	AX695965 Sequence
37	361	29.9	146327	9	AL162253	AL162253 Human DNA
38	330	27.3	401	6	BD275827	BD275827 COMPOUNDS
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